1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/927,112

DATE: 01/29/2002
TIME: 12:19:42

Input Set : D:\38155-20048.txt
Output Set: N:\CRF3\01292002\I927112.raw

p.5

ENTERED

03.20.02

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 4 <110> APPLICANT: Millennium Pharmaceuticals, Inc.
 5        Meyers, Rachel
 6        Silos-Santiago, Inmaculada
 8 <120> TITLE OF INVENTION: 32544, a novel human phospholipase C and
 9        uses thereof
11 <130> FILE REFERENCE: 38155-20048.00
13 <140> CURRENT APPLICATION NUMBER: US 09/927,112
14 <141> CURRENT FILING DATE: 2001-08-10
16 <150> PRIOR APPLICATION NUMBER: US 60/246,808
17 <151> PRIOR FILING DATE: 2000-11-08
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4635
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (435)...(4058)
32 <400> SEQUENCE: 1
33 tcgcgatcta gaactagtgg cacggctcct gcactcccac tgccgcagga actgctcagg      60
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35 gctgaggggc tgagtgctca ttccagccgc ctcggggaac ccgggctggg agaccccatg     180
36 cctggggggtg agcctggagc cagggcagtg cggtgagagg ctccggagag agggctgggc    240
37 accaccaggc ttgggtgtgt gatgcgctgc tggcccaggc tacaccccga caagggacac     300
38 cggggggccct gggagcagag agacctcaga gcagcctcct cctgcctcct gtggacggcc    360
39 ggccccagct ggtgatccca gccagtccca gctttcagtt gctgccccca ccgacagtcc     420
40 tcagtccctc catg atg gct ccc ccg aca gcc ggc ccc ctt cct ggc cca      470
41              Met Ala Pro Pro Thr Ala Gly Pro Leu Pro Gly Pro
42               1               5                  10
44 gct ctt ccg cct gag gac cca ggg ccg gat ccg gag agc agg tgg ctt      518
45 Ala Leu Pro Pro Glu Asp Pro Gly Pro Asp Pro Glu Ser Arg Trp Leu
46           15                20                25
48 ttc ttg agc gcc aac att ctg ccc gtg gtg gag cgg tgc atg ggt gcc      566
49 Phe Leu Ser Ala Asn Ile Leu Pro Val Val Glu Arg Cys Met Gly Ala
50        30                35                40
52 atg caa gag ggg atg cag atg gtg aag ctg cgt ggc ggc tcc aag ggc      614
53 Met Gln Glu Gly Met Gln Met Val Lys Leu Arg Gly Gly Ser Lys Gly
54 45                50                55                60
56 ctg gtc cgc ttc tac tac ctg gac gag cac cgc tcc tgc atc cgc tgg      662
57 Leu Val Arg Phe Tyr Tyr Leu Asp Glu His Arg Ser Cys Ile Arg Trp
58              65                70                75
60 agg ccc tca cgc aag aac gag aag gcc aag atc tcc atc gac tcc atc      710
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61 Arg Pro Ser Arg Lys Asn Glu Lys Ala Lys Ile Ser Ile Asp Ser Ile
62               80                  85                  90
64 cag gag gtg agt gag ggg cgg cag tcg gag gtc ttc cag cgc tac cct      758
65 Gln Glu Val Ser Glu Gly Arg Gln Ser Glu Val Phe Gln Arg Tyr Pro
66           95                 100                 105
68 gac ggc agc ttc gac ccc aac tgc tgc ttc agc atc tac cac ggc agc      806
69 Asp Gly Ser Phe Asp Pro Asn Cys Cys Phe Ser Ile Tyr His Gly Ser
70     110                 115                 120
72 cac cgc gag tcg ctg gac ctg gtc tcc acc agc agc gag gtg gcg cgc      854
73 His Arg Glu Ser Leu Asp Leu Val Ser Thr Ser Ser Glu Val Ala Arg
74 125                 130                 135                 140
76 acc tgg gtc act ggc ctg cgc tac ctc atg gcc ggc atc agc gac gag      902
77 Thr Trp Val Thr Gly Leu Arg Tyr Leu Met Ala Gly Ile Ser Asp Glu
78                 145                 150                 155
80 gac agc ctg gct cgc cgc cag cgc acc agg gac cag tgg ctg aag cag      950
81 Asp Ser Leu Ala Arg Arg Gln Arg Thr Arg Asp Gln Trp Leu Lys Gln
82             160                 165                 170
84 acg ttt gac gag gcc gac aag aac ggg gat ggc agc ctg agc att ggc      998
85 Thr Phe Asp Glu Ala Asp Lys Asn Gly Asp Gly Ser Leu Ser Ile Gly
86         175                 180                 185
88 gag gtc ctg cag ctg ctg cac aag ctc aac gtg aac ctg ccc cgg cag      1046
89 Glu Val Leu Gln Leu Leu His Lys Leu Asn Val Asn Leu Pro Arg Gln
90     190                 195                 200
92 agg gtg aag cag atg ttc agg gaa gcg gac acg gat gac cac caa ggg      1094
93 Arg Val Lys Gln Met Phe Arg Glu Ala Asp Thr Asp Asp His Gln Gly
94 205                 210                 215                 220
96 acg ctg ggt ttt gaa gag ttc tgt gcc ttc tac aag atg atg tcc acc      1142
97 Thr Leu Gly Phe Glu Glu Phe Cys Ala Phe Tyr Lys Met Met Ser Thr
98                 225                 230                 235
100 cgc cgg gac ctc tac ctg ctc atg ctg acc tac agc aac cac aag gac     1190
101 Arg Arg Asp Leu Tyr Leu Leu Met Leu Thr Tyr Ser Asn His Lys Asp
102             240                 245                 250
104 cac ctg gat gcc gcc agc ctg cag cgc ttc ctg cag gtg gag cag aag     1238
105 His Leu Asp Ala Ala Ser Leu Gln Arg Phe Leu Gln Val Glu Gln Lys
106         255                 260                 265
108 atg gcg ggt gtg acc ctc gag agc tgc cag gac atc atc gag cag ttt     1286
109 Met Ala Gly Val Thr Leu Glu Ser Cys Gln Asp Ile Ile Glu Gln Phe
110     270                 275                 280
112 gag cca tgc cca gaa aac aag agt aag ggg ctg ctg ggc att gat ggc     1334
113 Glu Pro Cys Pro Glu Asn Lys Ser Lys Gly Leu Leu Gly Ile Asp Gly
114 285                 290                 295                 300
116 ttc acc aac tac acc agg agc cct gct ggt gac atc ttc aac cct gag     1382
117 Phe Thr Asn Tyr Thr Arg Ser Pro Ala Gly Asp Ile Phe Asn Pro Glu
118                 305                 310                 315
120 cac cac cat gtg cac cag gac atg acg cag ccg ctg agc cac tac ttc     1430
121 His His His Val His Gln Asp Met Thr Gln Pro Leu Ser His Tyr Phe
122             320                 325                 330
124 atc acc tcg tcc cac aac acc tac ctc gtg ggt gac cag ctc atg tcc     1478
125 Ile Thr Ser Ser His Asn Thr Tyr Leu Val Gly Asp Gln Leu Met Ser
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126         335                    340                    345
128 cag tca cgg gtg gac atg tat gct tgg gtc ctg cag gct ggc tgc cgc    1526
129 Gln Ser Arg Val Asp Met Tyr Ala Trp Val Leu Gln Ala Gly Cys Arg
130     350                    355                    360
132 tgc gtg gag gtg gac tgc tgg gat ggg ccc gac ggg gag ccc att gtg    1574
133 Cys Val Glu Val Asp Cys Trp Asp Gly Pro Asp Gly Glu Pro Ile Val
134 365                    370                    375                    380
136 cac cat ggc tac act ctg act tcc aag atc ctc ttc aaa gac gtc att    1622
137 His His Gly Tyr Thr Leu Thr Ser Lys Ile Leu Phe Lys Asp Val Ile
138                    385                    390                    395
140 gaa acc atc aac aaa tat gcc ttc atc aag aat gag tac cca gtg atc    1670
141 Glu Thr Ile Asn Lys Tyr Ala Phe Ile Lys Asn Glu Tyr Pro Val Ile
142                    400                    405                    410
144 ctg tcc atc gaa aac cac tgc agt gtc atc cag cag aag aaa atg gcc    1718
145 Leu Ser Ile Glu Asn His Cys Ser Val Ile Gln Gln Lys Lys Met Ala
146         415                    420                    425
148 cag tat ctg act gac atc ctt ggg gac aag ctg gac ctg tca tca gtg    1766
149 Gln Tyr Leu Thr Asp Ile Leu Gly Asp Lys Leu Asp Leu Ser Ser Val
150     430                    435                    440
152 agc agt gaa gat gcc acc aca ctc ccc tct cca cag atg ctc aag ggc    1814
153 Ser Ser Glu Asp Ala Thr Thr Leu Pro Ser Pro Gln Met Leu Lys Gly
154 445                    450                    455                    460
156 aag atc ctc gtg aag ggg aag aag ctc cca gcc aac atc agc gag gat    1862
157 Lys Ile Leu Val Lys Gly Lys Lys Leu Pro Ala Asn Ile Ser Glu Asp
158                    465                    470                    475
160 gcg gag gaa ggc gag gtg tct gat gag gac agt gct gat gag att gac    1910
161 Ala Glu Glu Gly Glu Val Ser Asp Glu Asp Ser Ala Asp Glu Ile Asp
162         480                    485                    490
164 gat gac tgc aag ctc ctc aat ggg gat gca tcc acc aat cga aag cgt    1958
165 Asp Asp Cys Lys Leu Leu Asn Gly Asp Ala Ser Thr Asn Arg Lys Arg
166         495                    500                    505
168 gta gaa aac act gct aag agg aaa ctg gat tcc ctc atc aaa gag tcg    2006
169 Val Glu Asn Thr Ala Lys Arg Lys Leu Asp Ser Leu Ile Lys Glu Ser
170     510                    515                    520
172 aag att cgg gac tgt gag gac ccc aac aac ttc tcc gtc tcc aca ctg    2054
173 Lys Ile Arg Asp Cys Glu Asp Pro Asn Asn Phe Ser Val Ser Thr Leu
174 525                    530                    535         ·         540
176 tcc cca tct gga aag ctc gga cgc aag agc aag gct gaa gag gac gtg    2102
177 Ser Pro Ser Gly Lys Leu Gly Arg Lys Ser Lys Ala Glu Glu Asp Val
178                    545                    550                    555
180 gag tct ggg gag gat gcc ggg gcc agc aga cgc aat ggc cgc ctc gtc    2150
181 Glu Ser Gly Glu Asp Ala Gly Ala Ser Arg Arg Asn Gly Arg Leu Val
182                    560                    565                    570
184 gtg gga agc ttc tcc agg cgc aag aag aag ggc agc aag ctg aag aag    2198
185 Val Gly Ser Phe Ser Arg Arg Lys Lys Lys Gly Ser Lys Leu Lys Lys
186         575                    580                    585
188 gcg gcc agc gtg gag gag gga gat gag ggt cag gac tcc ccg gga ggc    2246
189 Ala Ala Ser Val Glu Glu Gly Asp Glu Gly Gln Asp Ser Pro Gly Gly
190     590                    595                    600
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192 cag agc cga ggg gcg acc cgg cag aag aag acc atg aag ctg tcc cgg    2294
193 Gln Ser Arg Gly Ala Thr Arg Gln Lys Lys Thr Met Lys Leu Ser Arg
194 605               610               615               620
196 gcc ctc tct gac ctg gtg aag tac acc aag tcc gtg gcc acc cac gac    2342
197 Ala Leu Ser Asp Leu Val Lys Tyr Thr Lys Ser Val Ala Thr His Asp
198               625               630               635
200 ata gag atg gag gcg gcg tcc agc tgg cag gtg tcg tcc ttc agc gag    2390
201 Ile Glu Met Glu Ala Ala Ser Ser Trp Gln Val Ser Ser Phe Ser Glu
202               640               645               650
204 acc aag gcc cac cag att ctg cag cag aag ccg gcg cag tac cta cgc    2438
205 Thr Lys Ala His Gln Ile Leu Gln Gln Lys Pro Ala Gln Tyr Leu Arg
206               655               660               665
208 ttc aac cag cag cag ctc tcc cgc atc tac ccc tcc tcc tac cgt gtg    2486
209 Phe Asn Gln Gln Gln Leu Ser Arg Ile Tyr Pro Ser Ser Tyr Arg Val
210     670               675               680
212 gac tcc agc aac tac aac ccg cag ccc ttc tgg aac gcc ggc tgc caa    2534
213 Asp Ser Ser Asn Tyr Asn Pro Gln Pro Phe Trp Asn Ala Gly Cys Gln
214 685               690               695               700
216 atg gtt gcc ctg aac tac cag tca gag ggg cgg atg ctg cag ctg aac    2582
217 Met Val Ala Leu Asn Tyr Gln Ser Glu Gly Arg Met Leu Gln Leu Asn
218               705               710               715
220 cga gcc aag ttc agc gcc aac ggt ggc tgc ggc tac gta ctc aag cct    2630
221 Arg Ala Lys Phe Ser Ala Asn Gly Gly Cys Gly Tyr Val Leu Lys Pro
222               720               725               730
224 ggg tgc atg tgc cag ggc gtg ttc aac ccc aac tcg gag gac ccc ctg    2678
225 Gly Cys Met Cys Gln Gly Val Phe Asn Pro Asn Ser Glu Asp Pro Leu
226               735               740               745
228 ccc ggg cag ctc aag aag cag ctg gtg ctc cgg atc atc agt ggc cag    2726
229 Pro Gly Gln Leu Lys Lys Gln Leu Val Leu Arg Ile Ile Ser Gly Gln
230     750               755               760
232 cag ctt ccc aag ccg cgc gac tcc atg ctg ggg gac cgt ggg gag atc    2774
233 Gln Leu Pro Lys Pro Arg Asp Ser Met Leu Gly Asp Arg Gly Glu Ile
234 765               770               775               780
236 atc gac ccc ttt gtg gag gtg gag atc att ggg ctc cct gtg gac tgc    2822
237 Ile Asp Pro Phe Val Glu Val Glu Ile Ile Gly Leu Pro Val Asp Cys
238               785               790               795
240 agc agg gag cag acc cgc gtg gtg gac gac aac ggg ttc aac ccc acc    2870
241 Ser Arg Glu Gln Thr Arg Val Val Asp Asp Asn Gly Phe Asn Pro Thr
242               800               805               810
244 tgg gag gag acc ctg gtt ttc atg gtg cac atg ccg gag atc gcg ctg    2918
245 Trp Glu Glu Thr Leu Val Phe Met Val His Met Pro Glu Ile Ala Leu
246               815               820               825
248 gtc cgc ttc ctc gtc tgg gac cac gat ccc atc ggg cgt gac ttc att    2966
249 Val Arg Phe Leu Val Trp Asp His Asp Pro Ile Gly Arg Asp Phe Ile
250     830               835               840
252 ggc cag agg acg ctg gcc ttc agc agc atg atg cca ggc tac aga cac    3014
253 Gly Gln Arg Thr Leu Ala Phe Ser Ser Met Met Pro Gly Tyr Arg His
254 845               850               855               860
256 gtg tac cta gaa ggg atg gaa gag gcc tcc atc ttc gtg cat gtg gct    3062
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257 Val Tyr Leu Glu Gly Met Glu Glu Ala Ser Ile Phe Val His Val Ala
258                   865             870             875
260 gtc agt gac atc agc ggt aag gtc aag cag gct ctg ggc cta aaa ggc     3110
261 Val Ser Asp Ile Ser Gly Lys Val Lys Gln Ala Leu Gly Leu Lys Gly
262                   880             885             890
264 ctc ttc ctc cga ggc cca aag ccc ggc tcg ctg gac agt cat gct gct     3158
265 Leu Phe Leu Arg Gly Pro Lys Pro Gly Ser Leu Asp Ser His Ala Ala
266             895             900             905
268 ggg cgg ccc ccg gcc cgg ccc tcc gtt agc cag cgg atc ctg cgg cgc     3206
269 Gly Arg Pro Pro Ala Arg Pro Ser Val Ser Gln Arg Ile Leu Arg Arg
270     910             915             920
272 acg gcc agc gcc ccg acc aag agc cag aag ccg ggc cgc agg ggc ttc     3254
273 Thr Ala Ser Ala Pro Thr Lys Ser Gln Lys Pro Gly Arg Arg Gly Phe
274 925             930             935             940
276 ccg gag ctg gtc ctg ggt aca cgg gac aca ggc tcc aag ggg gtg gca     3302
277 Pro Glu Leu Val Leu Gly Thr Arg Asp Thr Gly Ser Lys Gly Val Ala
278                   945             950             955
280 gac gat gtg gtg ccc ccc ggg ccc gga cct gct ccg gaa gcc cca gcc     3350
281 Asp Asp Val Val Pro Pro Gly Pro Gly Pro Ala Pro Glu Ala Pro Ala
282             960             965             970
284 cag gag ggg ccc ggc agc ggc agc ccc cga ggt aag gcg cca gct gcg     3398
285 Gln Glu Gly Pro Gly Ser Gly Ser Pro Arg Gly Lys Ala Pro Ala Ala
286         975             980             985
288 gtg gca gag aag agc cct gtg cga gtg cgg ccc ccg cgt gtc ctg gac     3446
289 Val Ala Glu Lys Ser Pro Val Arg Val Arg Pro Pro Arg Val Leu Asp
290     990             995             1000
292 ggc ccc ggg cct gct ggg atg gcc gcc aca tgc atg aag tgt gtg gtg     3494
293 Gly Pro Gly Pro Ala Gly Met Ala Ala Thr Cys Met Lys Cys Val Val
294 1005            1010            1015            1020
296 gga tcc tgc gcc ggc gtg aac acc ggg ggc ctg cag agg gag cgg cca     3542
297 Gly Ser Cys Ala Gly Val Asn Thr Gly Gly Leu Gln Arg Glu Arg Pro
298             1025            1030            1035
300 ccc agc ccg ggg cct gca agc agg cag gca gcc att cgc cag cag ccc     3590
301 Pro Ser Pro Gly Pro Ala Ser Arg Gln Ala Ala Ile Arg Gln Gln Pro
302             1040            1045            1050
304 cgg gcc cgg gct gac tca ctg ggg gcc ccc tgc tgt ggc ctg gac cct     3638
305 Arg Ala Arg Ala Asp Ser Leu Gly Ala Pro Cys Cys Gly Leu Asp Pro
306             1055            1060            1065
308 cac gct atc ccg ggg aga agc aga gag gcc ccc aag ggt cct ggg gcc     3686
309 His Ala Ile Pro Gly Arg Ser Arg Glu Ala Pro Lys Gly Pro Gly Ala
310     1070            1075            1080
312 tgg agg cag ggt cca ggc ggt agc ggc tcc atg tcc tcg gac tcc agc     3734
313 Trp Arg Gln Gly Pro Gly Gly Ser Gly Ser Met Ser Ser Asp Ser Ser
314 1085            1090            1095            1100
316 agc cca gac agc ccg ggc atc ccc gaa agg tcc ccc cgc tgg cct gag     3782
317 Ser Pro Asp Ser Pro Gly Ile Pro Glu Arg Ser Pro Arg Trp Pro Glu
318             1105            1110            1115
320 ggt gcc tgc agg caa ccg ggg gcc ctg cag gga gag atg agt gcc ttg     3830
321 Gly Ala Cys Arg Gln Pro Gly Ala Leu Gln Gly Glu Met Ser Ala Leu
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
→ explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/927,112

DATE: 01/29/2002
TIME: 12:19:43

Input Set : D:\38155-20048.txt
Output Set: N:\CRF3\01292002\I927112.raw

L:919 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17